

# SEQUENCE LISTING

<110> McCall, Catherine A.  
Tang, Liang  
Heska Corporation

<120> COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND  
CANINE IL-13 RECEPTORS

<130> AL-7

<140> not yet assigned

<141> 2001-04-09

<150> 60/195,659

<151> 2000-04-07

<150> 60/195,874

<151> 2000-04-07

<160> 104

<170> PatentIn Ver. 2.1

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5

10

15

cct

51

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gacaccacc atg gag tct gtg ttc tgc tgg gtt ttc ctt gtc gtt att tta 111  
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 1 5 10

aaa ggt gtc cag ggt gag gtg cag ttg gtg gag tct ggg gga gac ctg 159  
 Lys Gly Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu  
 15 20 25 30

gtg aag cct ggg ggg tcc ctg aga ctc tcc tgt gtg gcc tct gga ttc 207  
 Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe  
 35 40 45

acc ttc agt tcg tac tac atg cat tgg atc cgc cag gct cca ggg aag 255  
 Thr Phe Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys  
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ggg ctt cag cgg gtc gca cat att aga ggt gat gga agg act aca cac 303  
 Gly Leu Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His  
 65 70 75

T05040-566666





tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc 1503  
 Ser His Ser Pro Gly Lys  
 465

cccacccttg gctctcagga tcccctgagg acacctgagc cctgtccct gtgtacataa 1563

ccctgggtag gcacccatca tgaaataaag caccagcac tgcctgggc cctgcaaaaa 1623

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe  
 35 40 45

Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His Tyr Ala  
 65 70 75 80

Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr Ala Ile  
 100 105 110

Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser  
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Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val  
 145 150 155 160

098899:04001

Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val  
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Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser  
 180 185 190

Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val Thr Val  
 195 200 205

Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His  
 210 215 220

Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg  
 225 230 235 240

Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro  
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Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr  
 260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp  
 275 280 285

Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr  
 290 295 300

Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val  
 305 310 315 320

Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu  
 325 330 335

Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg  
 340 345 350

Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val  
 355 360 365

Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile  
 370 375 380

Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp  
 385 390 395 400

Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro  
 405 410 415

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Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser  
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Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val  
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Ser Pro Gly Lys  
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 tca 51  
 Ser

<210> 8  
 <211> 17  
 <212> PRT  
 <213> Canis familiaris

<400> 8  
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 1 5 10 15  
 Ser

<210> 9  
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 <212> DNA  
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<400> 9  
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 <213> Canis familiaris



<220>

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Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly

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10

15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg 152

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

20

25

30

35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat 200

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr

40

45

50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc 248

Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val

55

60

65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag 296

Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys

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75

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ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc 344

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu

85

90

95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg 392

Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val

100

105

110

115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat 440

Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn

120

125

130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt 488

Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val

135

140

145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc 536

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala

150

155

160

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc	584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser	
165 170 175	
tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc	632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val	
180 185 190 195	
ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc	680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro	
200 205 210	
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg	728
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro	
215 220 225	
gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc	776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys	
230 235 240	
aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg	824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser	
245 250 255	
gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga	872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg	
260 265 270 275	
aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct	920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro	
280 285 290	
gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc	968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala	
295 300 305	
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Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val	
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agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc	1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe	
325 330 335	
aag tgc aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act	1112
Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr	
340 345 350 355	

atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg	1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu	
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cca cca tcc cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc	1208
Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr	
375 380 385	
tgc ctg atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag	1256
Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln	
390 395 400	
agc aat gga cag ccg gag ccc gag agc aag tac cac acg act gcg ccc	1304
Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro	
405 410 415	
cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg	1352
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val	
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Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met	
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cat gaa gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct	1448
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Pro Gly Lys	
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 Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe  
 35 40 45



His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly  
 325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile  
 340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val  
 355 360 365

Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val  
 370 375 380

Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val  
 385 390 395 400

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr  
 405 410 415

Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys  
 420 425 430

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys  
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Ala Val Met His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu  
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Ser His Ser Pro Gly Lys  
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<210> 12

<211> 1460

<212> DNA

<213> Canis familiaris

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 Gly Cys Gly Leu  
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 <211> 20  
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Gly Cys Gly Leu  
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<220>  
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Val Phe Leu Val Ala Ile Leu Lys Gly Val Gln Gly Asp Val Gln Leu  
10 15 20

gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg tcc ttg aga ctg 148  
Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Arg Leu  
25 30 35

tcc tgt gtg gcc tct gga ttc acc ttt agt agc tgt gcc atg agc tgg 196  
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Cys Ala Met Ser Trp  
40 45 50 55

gtc cgt cag tct cca ggg aag ggg cct cag tgg gtc gca act att cgg 244  
Val Arg Gln Ser Pro Gly Lys Gly Pro Gln Trp Val Ala Thr Ile Arg  
60 65 70











Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp  
 435 440 445

Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr  
 450 455 460

Gln Ile Ser Leu Ser His Ser Pro Gly Lys  
 465 470

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 <212> DNA  
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 gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660  
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 acttccatca taccgaatag ttgcgacca ctgaggcccc ttccctggag actgacggac 1260  
 ccagctcatg gcacagctac taaaggtgaa tccagaggcc acacaggaca gtctcaagga 1320  
 cccccaggc ttcaccaggt ctccccaga ctccaccagc tgcacgtcac cctggacacc 1380  
 ctttaaaata gcgacaagga aaaccagta gagcacagac tccatggtgn tttgtctgtg 1440  
 ttgtgcctga gcactt 1456

<210> 19

<211> 1453  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (32)..(1450)

<400> 19  
 agtgctcagg acaccacaca gacaaatcac c atg gag tct gtg ctc ttc tgg 52  
 Met Glu Ser Val Leu Phe Trp  
 1 5

gtt ttc ctt gtc act att tta aaa ggt gtc cag ggt gag gta cgt ttg 100  
 Val Phe Leu Val Thr Ile Leu Lys Gly Val Gln Gly Glu Val Arg Leu  
 10 15 20

gtg gag tct gga gga acc ctg gtg aag cct ggg ggg tcc ctg aaa ctc 148  
 Val Glu Ser Gly Gly Thr Leu Val Lys Pro Gly Gly Ser Leu Lys Leu  
 25 30 35

tct tgt gtg gcc tct gga ttc acc ttc aga aga tac tcc atg gac tgg 196  
 Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Arg Tyr Ser Met Asp Trp  
 40 45 50 55

gtc cgc cag gct cca ggc aag agc ctg cag tgg gtc gcc ggg att aac 244  
 Val Arg Gln Ala Pro Gly Lys Ser Leu Gln Trp Val Ala Gly Ile Asn  
 60 65 70

ggg gat ggc aca gga aca tcc tat tca cag act gtg aag ggc cga ttc 292  
 Gly Asp Gly Thr Gly Thr Ser Tyr Ser Gln Thr Val Lys Gly Arg Phe  
 75 80 85

acc atc tcc aga gac aac gcc aag aac acc ctc tat ctg cag ata aac 340  
 Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Ile Asn  
 90 95 100

agc ctg aga gcc gaa gac tct gct gtg tat tat tgt gcc aag agc tgg 388  
 Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Ser Trp  
 105 110 115

tct cgt aat ggg gat ctt gac tac tgg ggc cag gga acc ctg gtc acc 436  
 Ser Arg Asn Gly Asp Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr  
 120 125 130 135

gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg gcc ccc 484  
 Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu Ala Pro  
 140 145 150



acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc gag agg acc 1108  
 Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Arg Thr  
 345 350 355

atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg 1156  
 Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu  
 360 365 370 375

ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc ttg aca tgc 1204  
 Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser Leu Thr Cys  
 380 385 390

ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc 1252  
 Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser  
 395 400 405

aat gga cag cag gag cct gag agc aag tac cgc acg acc ccg ccc cag 1300  
 Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln  
 410 415 420

ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac 1348  
 Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp  
 425 430 435

aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat 1396  
 Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His  
 440 445 450 455

gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc cat tct ccg 1444  
 Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro  
 460 465 470

ggt aaa tga 1453  
 Gly Lys

<210> 20  
 <211> 473  
 <212> PRT  
 <213> Canis familiaris

<400> 20  
 Met Glu Ser Val Leu Phe Trp Val Phe Leu Val Thr Ile Leu Lys Gly  
 1 5 10 15  
 Val Gln Gly Glu Val Arg Leu Val Glu Ser Gly Gly Thr Leu Val Lys  
 20 25 30







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<220>  
<221> CDS  
<222> (1) .. (66)
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<210> 23
<211> 22
<212> PRT
<213> Canis familiaris
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<400> 23

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys  
1 5 10 15

Cys Pro Ala Pro Glu Met  
20

<210> 24

<211> 66

<212> DNA

<213> Canis familiaris

<400> 24

catttcaggg gctgggcatt tgggacaatc aggtgggcga ggaactcttc cattttctct 60  
tttggg 66

<210> 25

<211> 938

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (37)..(753)

<220>

<223> At location 475, n = unknown

<400> 25

ggcacgaggg tccccagaag gcaggatcaa tcagtg atg tcc tcc gac atg gcc 54  
Met Ser Ser Asp Met Ala  
1 5

tgg tcc cct ctc ctc ctc aca ctc ctc gct cac tgc aca ggg tcc tgg 102  
Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly Ser Trp  
10 15 20

gcc cag gct gtg ttg aat cag ccg gcc tca gta tct ggg gcc ctg ggc 150  
Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala Leu Gly  
25 30 35

cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata 198  
Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile  
40 45 50

ttc ggt gtg aac tgg tac caa caa ctc cca gga aag gcc cct aca gtc	246
Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Thr Val	
55 60 65 70	
ctc gtg gac agt gat ggg gat cga ccc tca ggg gtc cct gac aga ttt	294
Leu Val Asp Ser Asp Gly Asp Arg Pro Ser Gly Val Pro Asp Arg Phe	
75 80 85	
tct ggc tcc agt tct ggc aac tca ggc acc ctg acc atc act ggg ctc	342
Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr Leu Thr Ile Thr Gly Leu	
90 95 100	
cag gct gag gac gag gct gat tat tac tgt cag tct gtt gat tcc acg	390
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Val Asp Ser Thr	
105 110 115	
ctt ggt gtt tac gtg ttc ggc tca gga acc caa ctg act gtc ctt ggt	438
Leu Gly Val Tyr Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly	
120 125 130	
cag ccc aag gcc tcc ccc tcg gtc aca ctc ttc ccg ncc tyc tyt gag	486
Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe Pro Xaa Xaa Xaa Glu	
135 140 145 150	
gag ctc ggc gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc	534
Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe	
155 160 165	
tac ccc arc ggc gtg acg gtg gcc tgg aag gca gac ggc agc ccc gtc	582
Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val	
170 175 180	
acc cag ggc gtg gag acc acc aag ccc tcc aag cag agc aac aac aag	630
Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys	
185 190 195	
tac gcg gcc agc agc tac ctg agc ctg acg cct gac aag tgg aaa tct	678
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Asp Lys Trp Lys Ser	
200 205 210	
cac agc agc ttc agc tgc ctg gtc acg cat gag ggg agc ccc gtg gaa	726
His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Pro Val Glu	
215 220 225 230	
aaa aag gtg gcc ccc gca aag tgc tct taggttcccg atgccccccg	773
Lys Lys Val Ala Pro Ala Lys Cys Ser	
235	

cccaccaaag ggggctcaaa gcctcaggac ctccaggagg atcttgctc ccatctgggt 833  
catcccagcc attccctta aaccaggca acattcaata aagtgttctt tcttcaatca 893  
gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 938

<210> 26  
<211> 239  
<212> PRT  
<213> Canis familiaris  
<223> At location 475, n = unknown

<400> 26  
Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala  
1 5 10 15  
His Cys Thr Gly Ser Trp Ala Gln Ala Val Leu Asn Gln Pro Ala Ser  
20 25 30  
Val Ser Gly Ala Leu Gly Gln Lys Val Thr Ile Ser Cys Ser Gly Asp  
35 40 45  
Thr Asn Asp Ile Asp Ile Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro  
50 55 60  
Gly Lys Ala Pro Thr Val Leu Val Asp Ser Asp Gly Asp Arg Pro Ser  
65 70 75 80  
Gly Val Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr  
85 90 95  
Leu Thr Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
100 105 110  
Gln Ser Val Asp Ser Thr Leu Gly Val Tyr Val Phe Gly Ser Gly Thr  
115 120 125  
Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ser Pro Ser Val Thr Leu  
130 135 140  
Phe Pro Xaa Xaa Xaa Glu Glu Leu Gly Ala Asn Lys Ala Thr Leu Val  
145 150 155 160  
Cys Leu Ile Ser Asp Phe Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys  
165 170 175  
Ala Asp Gly Ser Pro Val Thr Gln Gly Val Glu Thr Thr Lys Pro Ser

180

185

190

Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr  
195 200 205

Pro Asp Lys Trp Lys Ser His Ser Ser Phe Ser Cys Leu Val Thr His  
210 215 220

Glu Gly Ser Pro Val Glu Lys Lys Val Ala Pro Ala Lys Cys Ser  
225 230 235

<210> 27

<211> 938

<212> DNA

<213> Canis familiaris

<220>

<223> At location 464, n = unknown

<400> 27

tttttttttt tttttttttt tttttttttt tttttttttt ttttctgatt gaagaaagaa 60  
cactttattg aatgttgcc tgggtttaagg ggaatggctg ggatgacca gatgggaggc 120  
aagatcctcc tggaggtcct gaggttttga gccccctttg gtgggcgggg ggcacgaggc 180  
acctaagagc actttgcggg ggccaccttt ttttccacgg ggctccccctc atgcgtgacc 240  
aggcagctga agctgctgtg agatttccac ttgtcaggcg tcaggctcag gtagctgctg 300  
gccgcgtact tgttggtgct ctgcttgagg ggcttggtgg tctccacgcc ctgggtgacg 360  
gggctgccgt ctgccttcca ggccaccgtc acgccgytgg ggtagaagtc gctgatgagg 420  
cacaccaggg tggccttggt ggccgccgagc tcctcaragr aggnccggaa gagggtgacc 480  
gagggggagg ccttgggctg accaaggaca gtcagttggg ttcctgagcc gaacacgtaa 540  
acaccaagcg tggaatcaac agactgacag taataatcag cctcgtcctc agcctggagc 600  
ccagtgatgg tcagggtgcc tgagttgcca gaactggagc cagaaaatct gtcagggacc 660  
cctgagggtc gatcccatc actgtccacg aggactgtag gggcctttcc tgggagttgt 720  
tggtaccagt tcacaccgaa tatatcaatg tcattcgtgt ctccagagca ggagatggtg 780  
accttctggc ccagggtccc agatactgag gccggctgat tcaacacagc ctggggccag 840  
gaccctgtgc agtgagcgag gagggtgagg aggagagggg accaggccat gtcggaggac 900  
atcactgatt gatcctgcct tctggggacc ctctgtgc 938

<210> 28

<211> 578

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(423)

**THE**

<400> 28

31

<210> 29  
 <211> 141  
 <212> PRT  
 <213> Canis familiaris  
 <223> At locations 471, 481, 522 and 549, n = unknown

<400> 29  
 His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His  
     1                    5                    10                    15  
 Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly  
                     20                    25                    30  
 Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu  
                     35                    40                    45  
 Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe  
                     50                    55                    60  
 Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu  
                     65                    70                    75                    80  
 Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly  
                     85                    90                    95  
 Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln  
                     100                    105                    110  
 Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn  
                     115                    120                    125  
 His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys  
                     130                    135                    140

<210> 30  
 <211> 578  
 <212> DNA  
 <213> Canis familiaris  
 <220>  
 <223> At locations 30, 57, 98 and 108, n = unknown

<400> 30  
 tttttttttt gcaagggccc agggcagtggn tgggtgcttt atttcatgat ggggtgcntac 60  
 ccaggggttat gtacacaggg acaggggctc aggtgtcntc agggatcntg agagccaagg 120  
 gtgggggggct tgctgggtgc cgggcgtgtt gctcatttac ccggagaatg ggagagggat 180



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ttctgtgtgt agtgggtgtg tagagcttca tgcattcaccg cacatatgaa ggtgtctccc 240
cgctgccagc ggctcttgtc cacagagagc ttgctgtaca ggaagtagga cccgtcctcg 300
tccagctggg gcgggggtcgt gcgggtacttg ctctcaggct cctgctgtcc attgctctgc 360
cactccacat caatgtcagg tgggtagaag tcttttatca ggcagggtgat gctgactgtg 420
tcaactggatg acaactcctt tggggatggc ggcaggacat acacactggg cttatgggcc 480
ctccctctgg ccttagagat ggtcctctcg atgggagacg ggagggtctat gtggttgact 540
ctacatttga actccttacc attaaaccaa tcttgatg 578

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<210> 31
<211> 1364
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (59) .. (1183)

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<400> 31
ggcacgaggc cgattcacca tttccagaga caatgtcgag aacacgctgt atctgcag 58

atg aac agc ctg aga gct gag gat acg gcc ctg tat tac tgt aca agt 106
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
1 5 10 15

ggg tta tgg atc aac tgg tac ggt ccg aat ttt gac tcc tgg ggc cag 154
Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
20 25 30

gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt 202
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
35 40 45

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc 250
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
50 55 60

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc 298
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
65 70 75 80

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc 346
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
85 90 95

ctg cag tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc 394
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
100 105 110

```

[illegible]

gtg gag tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc 1018  
 Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg  
 305 310 315 320

acg acc ccg ccc cag ctg gag gag gac ggg tcc tac ttc ctg tac agc 1066  
 Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser  
 325 330 335

aag ctc tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata 1114  
 Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile  
 340 345 350

tgt gcg gtg atg cat gaa gct tta cac aac cac tac aca cag aaa tcc 1162  
 Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 355 360 365

ctc tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc 1213  
 Leu Ser His Ser Pro Gly Lys  
 370 375

cccacccttg gctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa 1273

ccccgggtag gcacctggca tgaaataaag caccagtagc tgccttgga aaaaaaaaaa 1333

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1364

<210> 32

<211> 375

<212> PRT

<213> Canis familiaris

<400> 32

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser  
 1 5 10 15

Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln  
 20 25 30

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val  
 35 40 45

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala  
 50 55 60

Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser  
 65 70 75 80



Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile  
 340 345 350

Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 355 360 365

Leu Ser His Ser Pro Gly Lys  
 370 375

<210> 33  
 <211> 1364  
 <212> DNA  
 <213> Canis familiaris

<400> 33  
 tttttttttt tttttttttt tttttttttt tttttttttt tttccagggc agtactgggt 60  
 gctttatttc atgccaggtg cctaccggg gttatgtaca cagggatggg ggctcaggca 120  
 tcctcatggg atcctgaaag ccaaggggtg ggggcttgct ggggtgccgg cgtgttgctc 180  
 atttaccgg agaatgggag agggatttct gtgtgtagtg gttgtgtaaa gcttcatgca 240  
 tcaccgcaca tatgaaggtg tctccccgct gccagcggct cttgtccaca gagagcttgc 300  
 tgtacaggaa gtaggaccg tcctcgtcca gctggggcgg ggtcgtgcgg tacttgctct 360  
 caggctcctg ctgtccattg ctctgccact ccacatcaat gtcaggtggg aagaagtctt 420  
 tgatcaggca tgtcaagctg actgtgttct tgctcaactc ctcccgggat ggcggcagga 480  
 catacacact gggttgatgg gcttgccctc tggccttgga gatggctctc tcgattgggg 540  
 atgggagggc tttgttggtg actttgcacg tgaactgctt ccccttgagc cagtcctggt 600  
 gcccgaatggg gaggacactg accacacggg aggtgccatt gaactgctcc tcacgaggct 660  
 gagtcttggc tgtttgcatc tgcttaccgt ccacgaacca gctgatctgc acctcagggt 720  
 cttctgggtc cagatccacc accacacatg tgacctcagg tgttcgggca atcaagaggg 780  
 tgtccttggg tttcggggga aagatgaaga ccgaaggccc tcccagcatt tcagggggtg 840  
 ggcatttggg acaatcaggt gggcgaggaa ctcttccatt ttctcttttg ggcactggct 900  
 tgtctacttt agttttgctg gccgggtggg ccacgttgca ggtgaaggct tcgctgggcc 960  
 acctgctgga gggcactgtc accatgctgc tgaggagta gagccctgag gactgcagga 1020  
 cggacgggaa ggtgtgcaca ccgctgggtc aggagccgga attccaggac acagttacag 1080  
 gctcggggaa gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc 1140  
 cgcagctggg ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gagacggtga 1200  
 ccagggttcc ctggccccag gagtcaaaat tcggaccgta ccagttgatc cataaccac 1260  
 ttgtacagta atacagggcc gtatcctcag ctctcaggct gttcatctgc agatacagcg 1320  
 tgttctcgac attgtctctg gaaatgggtga atcggcctcg tgcc 1364

<210> 34  
 <211> 1168  
 <212> DNA  
 <213> Canis familiaris

<220>

<221> CDS

<222> (48)..(1166)

<400> 34

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ccaggtgacc ccattcagtg ctcaggacac aacacagaca aaccacc atg gag tct      56
                                     Met Glu Ser
                                     1

gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt      104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
      5                      10                      15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg      152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
      20                      25                      30                      35

tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat      200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
                      40                      45                      50

ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc      248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val
                      55                      60                      65

gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag      296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys
      70                      75                      80

ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc      344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
      85                      90                      95

cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg      392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val
      100                      105                      110                      115

acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat      440
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn
                      120                      125                      130

ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt      488
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
                      135                      140                      145

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc      536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
      150                      155                      160
```







Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val  
 195 200 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val  
 210 215 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu  
 225 230 235 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg  
 260 265 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg  
 275 280 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val  
 290 295 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly  
 325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile  
 340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val  
 355 360 365

Tyr Val Leu Pro Pro  
 370

<210> 36

<211> 1168

<212> DNA

<213> Canis familiaris

<400> 36

gatggcggca ggacatacac actgggctga tgggcttgcc ctctggcttt ggagatagtc 60

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ctctcgatgg gggacggggg gcctatgtgg ttgactctgc acttgaactc ctttccggtg 120
agccagtcct ggtgctcaat ggggaggacg ctgaccacac ggtaggtgct gttgaactgc 180
tgctcacgag gctgctcttt ggctgtgtgc acctccttac catccacgaa ccagctgac 240
tgcacctcag ggtcctcacg gccagatct aacaccacac aggtgatctc ggggtgttcgg 300
gtaatcctga ggatgtcctt ggggtttcggg ggaaagatga agaccgaagg ccctcccagt 360
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tctacttttag tgttgctggc cgggtggacc acgttgccagg tgaaggctct gctggggccac 480
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<210> 37  
 <211> 1059  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1056)

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Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
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ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg 96
Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
      20             25             30

gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc 144
Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
      35             40             45

ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc 192
Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
      50             55             60

gac tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc 240

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85

90

95

Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn  
100 105 110

Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile  
115 120 125

Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile  
130 135 140

Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu  
145 150 155 160

Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln  
165 170 175

Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln  
180 185 190

Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu  
195 200 205

Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg  
210 215 220

Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys  
225 230 235 240

Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser  
245 250 255

Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile  
260 265 270

Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly  
275 280 285

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp  
290 295 300

Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser  
305 310 315 320

Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala  
325 330 335

Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys

<210> 39  
 <211> 1059  
 <212> DNA  
 <213> Canis familiaris

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 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180  
 ctggggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240  
 tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatgggtgg 300  
 caggacatac aactggggt gatgggcttg ccctctggct ttggagatag tcctctcgat 360  
 gggggacggg aggcctatgt ggttgactct gcaattgaac tcctttccgg tgagccagtc 420  
 ctggtgctca atggggagga cgctgaccac acggtaggtg ctggtgaact gctgctcacg 480  
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 agggctcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600  
 gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660  
 gactgggcat ggggatatac acttgacaggt ggactctttg ggcactggct tgtctacttt 720  
 agtggtgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga 780  
 gggcactgtc accgtgctgc tgagggagta gagccctgag gactgcagga cggacgggaa 840  
 ggtgtgcaca ccgctggtca aggagtcgga attccaggac acagttacag gctcggggaa 900  
 gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960  
 ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020  
 attgccccag tggtcatac cataataatg tcgcggcca 1059

<210> 40  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<220>  
 <223> At locations 15 and 21, n = unknown

<400> 40  
 caycargayt ggytnaaygg naargartty aartgy 36

<210> 41  
 <211> 28

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 41  
gccctccagc aggtggccca gcgagacc

28

<210> 42  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 42  
ggggatggcg gcaggacata cac

23

<210> 43  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 43  
tttaccgga gaatgggaga ggg

23

<210> 44  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 44  
ggtctgcgtg ggccacctgc tggagggc

28

<210> 45  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 45  
 ggggtgggggg cttgctgggt gccgggcg

28

<210> 46  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 46  
 ccaggtgacc ccattcagtg ctcaggacac

30

<210> 47  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 47  
 ctgtgtgacg ggagtatggc cgcgac

26

<210> 48  
 <211> 483  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <223> At location 470, n = unknown



<400> 48  
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 agtcattttg acaacaaaca ggataagaaa attgctcctg aaactcatcg ttcaaaagaa 120  
 gtaccctga atgagaggat ttgtctgcaa gtgggggtccc agtgcagcac caatgaaagt 180  
 gacaatccta gcattttggt ggaaaagtgc accccaccac ctgaaggtgg tcctgagtcg 240  
 gctgtgactg agctacaatg tgtttggcac aacctgagct acatgaagtg tacttggctt 300  
 cctggaagga atacaagccc tgacaccaac tatactctct actattggca cagcagcctg 360  
 ggaaaaattc ttcaatgcga agacatctat agagaaggtc aacacattgg ttgttccttt 420  
 gctctgacta atttgaagga ttccagtttt gaacaacaca gtgtccagan gatggtcaag 480  
 gtt 483

<210> 49  
 <211> 1547  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1215)

<400> 49  
 ggc ggg gtc gcc gca ccc acc gaa act cag cca cct gtg acg aat ttg 48  
 Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu  
 1 5 10 15  
 agt gtt tct gtt gaa aac ctc tgc acg gtc ata tgg aca tgg aac cct 96  
 Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro  
 20 25 30  
 ccc gag gga gcc agc ccg aat tgc acc tta cgg tat ttt agt cat ttt 144  
 Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe  
 35 40 45  
 gac aac aaa cag gat aag aaa att gct cct gaa act cat cgt tca aaa 192  
 Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys  
 50 55 60  
 gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag tgc 240  
 Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys  
 65 70 75 80  
 agc acc aat gaa agt gac aat cct agc att ttg gtg gaa aag tgc acc 288  
 Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr  
 85 90 95  
 cca cca cct gaa ggt gat cct gag tcg gct gtg act gag cta caa tgt 336

Pro	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	Glu	Leu	Gln	Cys	
			100					105					110			
gtt	tgg	cac	aac	ctg	agc	tac	atg	aag	tgt	act	tgg	ctt	cct	gga	agg	384
Val	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Thr	Trp	Leu	Pro	Gly	Arg	
		115					120					125				
aat	aca	agc	cct	gac	acc	aac	tat	act	ctc	tac	tat	tgg	cac	agc	agc	432
Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	Tyr	Trp	His	Ser	Ser	
	130					135					140					
ctg	gga	aaa	att	ctt	caa	tgc	gaa	gac	atc	tat	aga	gaa	ggt	caa	cac	480
Leu	Gly	Lys	Ile	Leu	Gln	Cys	Glu	Asp	Ile	Tyr	Arg	Glu	Gly	Gln	His	
145					150					155					160	
att	ggt	tgt	tcc	ttt	gct	ctg	act	aat	ttg	aag	gat	tcc	agt	ttt	gaa	528
Ile	Gly	Cys	Ser	Phe	Ala	Leu	Thr	Asn	Leu	Lys	Asp	Ser	Ser	Phe	Glu	
			165					170						175		
caa	cac	agt	gtc	caa	ata	atg	gtc	aag	gat	aat	gca	aga	aaa	att	aga	576
Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Arg	Lys	Ile	Arg	
		180						185				190				
ccg	tcc	ttc	aat	ata	gtg	cct	tta	act	tct	cat	gtg	aaa	cct	gat	ccc	624
Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	His	Val	Lys	Pro	Asp	Pro	
	195						200					205				
ccc	cat	att	aag	cgt	ctc	ttc	ttc	caa	aat	ggt	aac	ttg	tat	gtg	caa	672
Pro	His	Ile	Lys	Arg	Leu	Phe	Phe	Gln	Asn	Gly	Asn	Leu	Tyr	Val	Gln	
	210					215					220					
tgg	aag	aat	cca	caa	aat	ttt	tat	agc	aga	tgc	tta	tct	tac	caa	gta	720
Trp	Lys	Asn	Pro	Gln	Asn	Phe	Tyr	Ser	Arg	Cys	Leu	Ser	Tyr	Gln	Val	
225					230					235					240	
gaa	gtc	aat	aac	agc	cag	act	gag	acg	aat	gat	ata	ttc	tac	gtt	gaa	768
Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	Asn	Asp	Ile	Phe	Tyr	Val	Glu	
			245					250						255		
gaa	gcc	aaa	tgt	cag	aat	tca	gaa	ttt	gag	gga	aac	ctg	gag	ggt	aca	816
Glu	Ala	Lys	Cys	Gln	Asn	Ser	Glu	Phe	Glu	Gly	Asn	Leu	Glu	Gly	Thr	
		260						265				270				
att	tgt	ttc	atg	gtc	ccc	ggc	gtt	ctt	cct	gat	act	ttg	aac	aca	gtc	864
Ile	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	Thr	Leu	Asn	Thr	Val	
		275					280					285				
aga	ata	aga	gtc	aga	aca	aat	aag	tta	tgc	tat	gag	gat	gac	aaa	ctc	912

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu  
 290 295 300

tgg agt aat tgg agt caa gcg atg agt ata ggt gag aat acc gac ccc 960  
 Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro  
 305 310 315 320

acg ttc tat ata acc atg ttg ctc gcc act caa gtc atc gtt gca ggt 1008  
 Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly  
 325 330 335

gcc atc ata atc ctt ctg ctt tat ctc aaa agg ctc aag atc att ata 1056  
 Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile  
 340 345 350

ttc cct cca att cct gat cct ggc aag att ttt aaa gaa atg ttt gga 1104  
 Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly  
 355 360 365

gac cag aat gat gat acg ctg cac tgg agg aag tac gac atc tat gag 1152  
 Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu  
 370 375 380

aag caa aca aaa gaa gaa acg gac tca gta gtg ctg att gaa aac ctg 1200  
 Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu  
 385 390 395 400

aag aaa gcc tct cag taatggggat aacttatttt agccttcagc atgaccttgt 1255  
 Lys Lys Ala Ser Gln  
 405

aaagattcat cccacgttc tcgggaagct tcaaggtcaa gcatccttggg aaaggacatt 1315

acagtttcta cagcatgggtg tacctgggca tctccgacta cttcttcaac acagcagggc 1375

ttgtgtacca agaggcaggg gccttaaaca tgaccatcac ggacgacatg ataccaaaga 1435

aatccaaatt ccgactgaca accgattttt tggggaccct cataccccaa gtggccgaga 1495

tgttccccaa catgacgggt caattcaacg tctgggcctc ctccccgccg ca 1547

<210> 50  
 <211> 405  
 <212> PRT  
 <213> Canis familiaris

<400> 50



Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr  
 260 265 270

Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val  
 275 280 285

Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu  
 290 295 300

Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro  
 305 310 315 320

Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly  
 325 330 335

Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile  
 340 345 350

Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly  
 355 360 365

Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu  
 370 375 380

Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu  
 385 390 395 400

Lys Lys Ala Ser Gln  
 405

<210> 51  
 <211> 1547  
 <212> DNA  
 <213> Canis familiaris

<400> 51  
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 atcatgtcgt ccgtgatggt catgtttaag gccctgcct cttggtacac aagccctgct 180  
 gtgttgaaga agtagtcgga gatgccagg tacaccatgc tgtagaaact gtaatgtcct 240  
 ttccaagat gcttgacctt gaagcttccc gagaacgtgg ggatgaatct ttacaaggctc 300  
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 tgcagcgtat catcattctg gtctccaaac atttctttaa aaatcttgcc aggatcagga 480  
 attggaggga atataatgat cttgagcctt ttgagataaa gcagaaggat tatgatggca 540  
 cctgcaacga tgacttgagt ggcgagcaac atggttatat agaacgtggg gtcggtattc 600

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atgaaacaaa ttgtaccctc caggtttccc tcaaattctg aattctgaca tttggcttct 780
tcaacgtaga atatatcatt cgtctcagtc tggctgttat tgacttctac ttggtaagat 840
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gctccctcgg gaggggtcca tgtccatatg accgtgcaga ggttttcaac agaaacactc 1500
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<210> 52
<211> 1215
<212> DNA
<213> Canis familiaris

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<400> 52
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accttacggt attttagtca ttttgacaac aaacaggata agaaaattgc tcctgaaact 180
catcgttcaa aagaagtacc cctgaatgag aggatttgtc tgcaagtggg gtcccagtcg 240
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ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttctctg aaggaatata agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattcttcaa tgcaagaca tctatagaga aggtcaacac 480
attggttgtt cttttgctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt cttcaatat agtgccttta 600
acttctcatg tgaaacctga tcccccccat attagcgtc tcttcttcca aaatggtaac 660
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gaagtcaata acagccagac tgagacgaat gatataattc acgttgaaga agccaaatgt 780
cagaattcag aatttgaggg aaacctggag ggtacaattt gtttcatggt ccccggcgtt 840
cttctgata ctttgaacac agtcagaata agagtcagaa caaataagtt atgctatgag 900
gatgacaaac tctggagtaa ttggagtcaa gcgatgagta taggtgagaa taccgacccc 960
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cttctgcttt atctcaaaag gctcaagatc attatattcc ctccaattcc tgatcctggc 1080
aagattttta aagaaatgtt tggagaccag aatgatgata cgctgcactg gaggaagtac 1140
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aagaaagcct ctacg 1215

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<210> 53

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<211> 1215  
 <212> DNA  
 <213> Canis familiaris

<400> 53  
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 ttcttttaaaa atcttgccag gatcaggaat tggagggaat ataatgatct tgagcctttt 180  
 gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat 240  
 gggttatatag aacgtggggg cgggtattctc acctatactc atcgcttgac tccaattact 300  
 ccagagtttg tcatcctcat agcataactt atttgttctg actcttattc tgactgtgtt 360  
 caaagtatca ggaagaacgc cggggaccat gaaacaaatt gtaccctcca gggttccctc 420  
 aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtctg 480  
 gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt 540  
 ccattgcaca tacaagttac ctttttgga gaagagacgc ttaatatggg ggggatcagg 600  
 tttcacatga gaagttaaag gcactatatt gaaggacggg ctaatttttc ttgcattatc 660  
 cttgaccatt atttggacac tgtgttgttc aaaactggaa tccttcaa at tagtcagagc 720  
 aaaggaacaa ccaatgtgtt gaccttctct atagatgtct tcgcattgaa gaatttttcc 780  
 caggctgtctg tgccaatagt agagagtata gttggtgtca gggcttgtat tccttccagg 840  
 aagccaagta cacttcatgt agctcagggt gtgccaaaca cattgtagct cagtcacagc 900  
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 actttcattg gtgctgcact gggacccac ttgcagacaa atcctctcat tcaggggtac 1020  
 ttcttttgaa cgatgagttt caggagcaat tttcttatcc tgtttgttgt caaaatgact 1080  
 aaaataccgt aaggtgcaat tcgggctggc tccttcggga gggttccatg tccatagac 1140  
 cgtgcagagg ttttcaacag aaacactcaa attcgtcaca ggtggctgag tttcgggtggg 1200  
 tgcggcgacc ccgcc 1215

<210> 54  
 <211> 620  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (184)..(618)

<400> 54  
 ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60  
 aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120  
 taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180  
 gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228  
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu  
 1 5 10 15

gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276  
 Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val  
                   20                                  25                                  30

aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324  
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
                   35                                  40                                  45

ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372  
 Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu  
                   50                                  55                                  60

tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac 420  
 Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn  
                   65                                  70                                  75

tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat 468  
 Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp  
                   80                                  85                                  90                                  95

ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa 516  
 Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln  
                                   100                                  105                                  110

tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat 564  
 Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr  
                   115                                  120                                  125

tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac 612  
 Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp  
                   130                                  135                                  140

tgt gta ta 620  
 Cys Val  
                   145

<210> 55  
 <211> 145  
 <212> PRT  
 <213> Canis familiaris

<400> 55  
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val  
           1                                  5                                  10                                  15  
 Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn  
                   20                                  25                                  30



Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu  
 35 40 45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys  
 50 55 60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp  
 65 70 75 80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu  
 85 90 95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys  
 100 105 110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp  
 115 120 125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys  
 130 135 140

Val  
 145

<210> 56  
 <211> 620  
 <212> DNA  
 <213> Canis familiaris

<400> 56  
 tatacacagt ccatatcttg aatttttagtt tcccgatttc cttgtggtga tgtccaataa 60  
 gtagtttctg cccatgaact tctaacttct gatccatttg tgcattgtgc tggcagaagt 120  
 gtggtttatct ttgcttcaat acctttgtta agatcaaacc catctttgta atgtagattc 180  
 ttggtaatga tggctcttcca gttttcacta tcaatgtttc ggtattttta ttcattattct 240  
 attgtgcatt ccttaaaatt atccggaaat aatggagggt gccattgcaa agagagataa 300  
 cctaaatata caggggtccac tatctcaaaa tcttgaggag gattaacttt tatctcagca 360  
 ttgaaagca tagagccaaa tgctgtgcaa acaagcaggg tatagaggaa tccgacatcc 420  
 aatgaatga aagccatttc tccaagattc aatactttga agtttccact caataatatg 480  
 gtttctcaag aatgaatta tcataggcaa ttatcacagg tcctcttttt tttctcttct 540  
 ccagtttgga gacattaatt agaattctta agacttcctt tcctgtctga taatcaagca 600  
 cacaaactca gcctcgtgcc 620

<210> 57  
 <211> 878

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(765)

<220>

<223> At location 862, n = unknown

<400> 57

caa gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac	48
Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr	
1 5 10 15	
aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat	96
Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His	
20 25 30	
ttt gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat	144
Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His	
35 40 45	
tca gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga	192
Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly	
50 55 60	
tgc agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc	240
Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile	
65 70 75 80	
tgt gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt	288
Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe	
85 90 95	
att ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt	336
Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu	
100 105 110	
agt ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg	384
Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met	
115 120 125	
cct aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc	432
Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe	
130 135 140	
aca gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata	480



Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly  
 50 55 60

Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile  
 65 70 75 80

Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe  
 85 90 95

Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu  
 100 105 110

Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met  
 115 120 125

Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe  
 130 135 140

Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile  
 145 150 155 160

Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val  
 165 170 175

Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu  
 180 185 190

Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu  
 195 200 205

Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val  
 210 215 220

Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile  
 225 230 235 240

Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys  
 245 250 255

<210> 59

<211> 878

<212> DNA

<213> Canis familiaris

<400> 59

tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60

ttaataagac tcatatTTTaa catctggcca taagactgaa agttactgag tcaacagaat 120  
 gtgtcttgat gagaaaagac ttctTTTTTT gtatgaaaga tcgttttcag taaagccctt 180  
 tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaattggt 240  
 atcaagaaaa atactaaggt ttcttcccat atgtcacctt tccagcattg ttcactcctc 300  
 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360  
 cataatTTTT ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420  
 gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480  
 atgggtcctt taggcatggt ccatttcagg ttaatttctt ctgaattctt cacagtaaga 540  
 ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600  
 ggtctgatag gctgggattc tgatgacca ttaacacaga tgtagaaatc tttatagtct 660  
 gatgactcca aatagggaaa cctgcattcc atattttttc cattaacctt gatgtaatca 720  
 gtacactctg ctgaatgggc caagccctca taccagtaaa acaactggta attggtatca 780  
 aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatatata 840  
 cagtccatat cttgaatTTT agtttcccga tttccttg 878

<210> 60  
 <211> 1454  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (184)..(1341)  
  
 <220>  
 <223> At location 1438, n = unknown

<400> 60  
 ggcacgaggc tgagtttgtg tgcttgatta tcagacagga agggaagtct tagagattct 60  
  
 aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120  
  
 taattcattt cttgagaaac catattattg agtggaaact tcaaagtatt gaatcttgga 180  
  
 gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228  
 Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu  
 1 5 10 15  
  
 gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276  
 Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val  
 20 25 30  
  
 aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324  
 Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr  
 35 40 45  
  
 ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372





[illegible]Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val  
1 5 10 15

Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu  
35 40 45

Thr	Ile	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp
65					70					75					80

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys  
100 105 110

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys  
130 135 140

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly  
165 170 175

Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp  
195 200 205

Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro  
225 230 235 240



Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys  
 245 250 255

Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu  
 260 265 270

Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu  
 275 280 285

Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys  
 290 295 300

Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile  
 305 310 315 320

Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys  
 325 330 335

Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe  
 340 345 350

Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu  
 355 360 365

Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr  
 370 375 380

Phe Cys  
 385

<210> 62

<211> 1454

<212> DNA

<213> Canis familiaris

<220>

<223> At location 17, n = unknown

<400> 62

tttttttttt tttttcnttt taaaataaga tttattcaat atttgaggaa aagcttcagt 60  
 ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120  
 gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180  
 tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaattgt 240  
 atcaagaaaa atactaaggt ttccttccat atgtcacctt tccagcattg ttcactcactc 300  
 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360  
 cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420



<210> 64  
 <211> 1158  
 <212> DNA  
 <213> Canis familiaris

<400> 64  
 acagaatgtg tcttgatgag aaaagacttc tttttttgta tgaaagatcg ttttcagtaa 60  
 agccctttgc ttatacaaaa gcaggcaagt tattaccaaa acaaattattg agacaaaagc 120  
 aaatgggtatc aagaaaaata ctaagggtttc cttccatattg tcacctttcc agcattgttc 180  
 atcaactccac tcaactccaga ttccatcatc tgagcaataa atattcactt tactttcttac 240  
 caaaaagcat aattttttggc tttcatttga tgttcttggtg atttgtatct cattctcaac 300  
 tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360  
 ggctggaatg ggtccttttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420  
 agtaagacta aggtagtctg gtggcatagg ttttaactata ttttgaagct gaaaaataaa 480  
 atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540  
 atagtctgat gactccaaat agggaaacct gcattccata ttttttccat taaccttgat 600  
 gtaatcagta cactctgctg aatgggtccaa gccctcatac cagtaaaaca actggtaatt 660  
 ggtatcaaaa tggacaccca tgccagggtt ccaagagcag actaaatatt gccagttgta 720  
 atatacacag tccatatctt gaatttttagt ttcccgattt ccttgtgggtg atgtccaata 780  
 agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840  
 tgtgtttatc tttgcttcaa tacctttggt aagatcaaac ccatctttgt aatgtagatt 900  
 cttggtaatg atgggtcttc agttttcact atcaatgttt cggatatttt attcatattc 960  
 tattgtgcat tccttaaaat tatccggaaa taatggaggt tgccattgca aagagagata 1020  
 acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080  
 atttgaaagc atagagccaa atgctgtgca aacaagcagg gtatagagga atccgacatc 1140  
 caaatgaatg aaagccat 1158

<210> 65  
 <211> 1095  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1095)

<400> 65  
 tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat ttt 48  
 Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe  
 1 5 10 15  
 gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg caa 96  
 Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln  
 20 25 30  
 cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat gaa 144  
 Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

45

act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct aaa 720  
Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys

225	230	235	240	
gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca gag				768
Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu				
	245	250	255	
gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa atc				816
Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile				
	260	265	270	
aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga agt				864
Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser				
	275	280	285	
aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg agt				912
Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser				
	290	295	300	
gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta gta ttt				960
Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe				
305	310	315	320	
ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta ata act				1008
Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr				
	325	330	335	
tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc ttt cat				1056
Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His				
	340	345	350	
aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt				1095
Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys				
	355	360	365	

<210> 66

<211> 365

<212> PRT

<213> Canis familiaris

<400> 66

Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
1 5 10 15

Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
20 25 30

Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

45

Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu  
65 70 75 80

Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu  
85 90 95

Val	Arg	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Thr	Ser	Pro	Gln	Gly
			100					105					110		

Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp  
115 120 125

Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp  
130 135 140

Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala  
145 150 155 160

Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg  
165 170 175

Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val  
180 185 190

Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe  
195 200 205

Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu  
210 215 220

Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys  
225 230 235 240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu  
245 250 255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile  
260 265 270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser  
275 280 285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser

290

295

300

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe  
 305 310 315 320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr  
 325 330 335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His  
 340 345 350

Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys  
 355 360 365

&lt;210&gt; 67

&lt;211&gt; 1095

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 67

acagaatgtg tcttgatgag aaaagacttc tttttttgta tgaaagatcg ttttcagtaa 60  
 agccctttgc ttatacaaaa gcaggcaagt tattaccaa acaaattattg agacaaaagc 120  
 aaatgggtatc aagaaaaata ctaagggtttc cttccatattg tcacctttcc agcattgttc 180  
 atcactccac tcaactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240  
 caaaaagcat aattttttggc tttcatttga tgttcttggtg atttgtatct cattctcaac 300  
 tgtggttagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360  
 ggctggaatg ggtccttttag gcatgttcca tttcaggtta atttcctctg aattcttcac 420  
 agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480  
 atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540  
 atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600  
 gtaatcagta cactctgctg aatgggtcaa gccctcatc cagtaaaaca actggtaatt 660  
 ggtatcaaaa tggacacca tgccagggtt ccaagagcag actaaatatt gccagttgta 720  
 atatacacag tccatatctt gaatttttagt ttcccgattt ccttgtggtg atgtccaata 780  
 agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840  
 tgtgtttatc tttgcttcaa tacctttggt aagatcaaac ccatctttgt aatgtagatt 900  
 cttggtaatg atggctcttc agttttcact atcaatgttt cggatatttt attcatattc 960  
 tattgtgcat tccttaaaat tatccgaaa taatggaggt tgccattgca aagagagata 1020  
 acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080  
 atttgaaagc ataga 1095

&lt;210&gt; 68

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

<220>

<221> CDS

<222> (1)..(954)

<400> 68

atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat 48  
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp  
1 5 10 15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96  
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144  
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192  
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240  
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
65 70 75 80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288  
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
85 90 95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336  
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
100 105 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384  
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
115 120 125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432  
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe  
130 135 140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca 480  
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser  
145 150 155 160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc 528  
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys  
165 170 175







275

280

285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp  
 290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr  
 305 310 315

&lt;210&gt; 70

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 70

ggtttccttc cagatatcac ctttccagca ttgttcatca ctccactcac tccagattcc 60  
 atcatctgag caataaatat tcactttact tcttaccaaa aagcataatt tttggctttc 120  
 atttgatgtt cttgtgattt gtatctcatt ctcaactgtg gtagtcaccc aagtagtacc 180  
 atcctctgtg aattcaattt cataaatgaa acatttggct ggaatgggtc ctttaggcat 240  
 gttccatttc aggttaattt cctctgaatt cttcacagta agactaaggt agtctggtgg 300  
 catagggtta actatatttt gaagctgaaa aataaaatag ctgggtctga taggctggga 360  
 ttctgatgac ccattaacac agatgtagaa atctttatag tctgatgact ccaaataagg 420  
 aaacctgcat cccatatttt ttccattaac cttgatgtaa tcagtacact ctgctgaatg 480  
 gtccaagccc tcataccagt aaaacaactg gtaattggta tcaaaatgga cacccatgcc 540  
 aggtttccaa gagcagacta aatattgcc a gttgtaatat acacagtcca tatcttgaat 600  
 tttagtttcc cgatttcctt gtgggtgatgt ccaataagta gtttctgccc atgaacttct 660  
 aacttctgat ccatttgtgc attgtgctgg cagaagtgtg tttatctttg cttcaatacc 720  
 tttgttaaga tcaaaccat ctttghtaatg tagattcttg gtaatgatgg tcttccagtt 780  
 ttcactatca atgtttcggg attttaattc atattctatt gtgcattcct taaaattatc 840  
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 ctcaaaatcc tgaggaggat taacttttat ctcagcattt gaaagcatag acat 954

&lt;210&gt; 71

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1683)

&lt;400&gt; 71

atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat 48  
 Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp  
 1 5 10 15

ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg	96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
20 25 30	
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile	
50 55 60	
acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att	240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile	
65 70 75 80	
gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca	288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser	
85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
165 170 175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
195 200 205	





<400> 72

Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp  
1 5 10 15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
20 25 30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe  
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser  
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys  
165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys  
180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile  
195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser  
210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro  
225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr

245

250

255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln  
260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg  
275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp  
290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser  
305 310 315 320

Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp  
325 330 335

Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu  
340 345 350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro  
355 360 365

Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val  
370 375 380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr  
385 390 395 400

Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val  
405 410 415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys  
420 425 430

Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser  
435 440 445

Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro  
450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu  
465 470 475 480

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn  
485 490 495

Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu



500

505

510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys  
 515 520 525

Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu  
 530 535 540

Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly  
 545 550 555 560

Lys

&lt;210&gt; 73

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 73

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 catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttgtcca cagagagctt 120  
 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcatgc ggtgcttcc 180  
 ctcgggctcc tgctgtccat tgctctgcca ctccacatca atgtcagggtg ggtagaagtc 240  
 ttttatcagg caggtgatgc tgactgtgtc actggatgac aactcctttg gggatggcgg 300  
 caggacatac acactgggct tatgggacct ccctctggcc ttagagatgg tcctctcgat 360  
 gggagacggg aggtctatgt ggttgactct gcacttgaac tccttccctg tgagccagtc 420  
 ctggtgctca atggggagga cgctgaccac acggtaggtg ccgttgaact gctgctcacg 480  
 agactgggtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540  
 agggctcctca cggcccagat ctaacaccac acaggtgacc tcgggtgttc gggtaatcct 600  
 gaggatgtcc ttgggtttcg ggggaaagat gaggaccgaa ggccctcca gaggttcagg 660  
 gactgggcat gggggtgtat cagtgcactc gcattcattg aacctggct tgtctacttt 720  
 agtgttggat ccggtttcct tccagatata acctttccag cattgttcat cactccactc 780  
 actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840  
 tttttggctt tcatttgatg ttcttgtgat ttgtatctca ttctcaactg tggtagtcac 900  
 ccaagtagta ccactctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960  
 tccttttaggc atgttccatt tcagggttaat ttctctgaa ttcttcacag taagactaag 1020  
 gtagtctggg ggcatagggt taactatatt ttgaagctga aaaataaaat agctgggtct 1080  
 gataggctgg gattctgatg acccatatac acagatgtag aaatctttat agtctgatga 1140  
 ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200  
 ctctgctgaa tgggtccaagc cctcatacca gtaaaacaac tggtaattgg tatcaaaatg 1260  
 gacacccatg ccagggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320  
 catatcttga attttagttt cccgatttcc ttgtgggtgat gtccaataag tagtttctgc 1380  
 ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440  
 tgcttcaata cttttgttaa gatcaaacc atctttgtaa tgtagattct tggtaatgat 1500  
 ggtcttccag ttttactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560

cttaaaatta tccggaata atggaggttg ccattgcaaa gagagataac ctāaatatcc 1620  
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 agacat 1686

<210> 74  
 <211> 1698  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1695)

<400> 74  
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 Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp  
 1 5 10 15  
 ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96  
 Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
 20 25 30  
 caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144  
 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
 35 40 45  
 gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192  
 Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
 50 55 60  
 acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240  
 Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
 65 70 75 80  
 gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288  
 Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
 85 90 95  
 gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336  
 Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
 100 105 110  
 gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384  
 Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
 115 120 125  
 tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432

TC6040:5663360



Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val	
325 330 335	
cct cgc cca cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga	1056
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly	
340 345 350	
ggg cct tgc gtc ttc atc ttt ccc ccg aaa ccc aag gac acc ctg ttg	1104
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu	
355 360 365	
att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg gac cca	1152
Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro	
370 375 380	
gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag cag atg	1200
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met	
385 390 395 400	
caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc acc tac	1248
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr	
405 410 415	
cgt gtg gtc agt gtc ctg ccc att ggg cac cag gac tgg ctg aag ggg	1296
Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly	
420 425 430	
aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctg cca tcc ccg atc	1344
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile	
435 440 445	
gag agg acc atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg	1392
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val	
450 455 460	
tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc	1440
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser	
465 470 475 480	
ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag	1488
Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu	
485 490 495	
tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc acg acc	1536
Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr	
500 505 510	
ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctg	1584

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu  
 515 520 525

tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg 1632  
 Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala  
 530 535 540

gtg atg cat gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc 1680  
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser  
 545 550 555 560

cat tct ccg ggt aaa tga 1698  
 His Ser Pro Gly Lys  
 565

<210> 75  
 <211> 565  
 <212> PRT  
 <213> Canis familiaris

<400> 75  
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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
 65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
 100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe  
 130 135 140



Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr  
405 410 415

Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly  
420 425 430

Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile  
435 440 445

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val  
450 455 460

Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser  
465 470 475 480

Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu  
485 490 495

Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr  
500 505 510

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu  
515 520 525

Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala  
530 535 540

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser  
545 550 555 560

His Ser Pro Gly Lys  
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<210> 76

<211> 1698

<212> DNA

<213> Canis familiaris

<400> 76

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tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300  
gacatacaca ctgggctgat gggcttgccc tctggccttg gagatgggtcc tctcgatcgg 360

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acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1680
atttgaaagc atagacat                                     1698

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<210> 77  
 <211> 1692  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1689)

<400> 77

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg	96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
20 25 30	
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192







TC060710: 53532360

Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	Pro	Ile	Glu	Glu		
		435					440					445					
atc	atc	tcc	aag	acc	cca	ggg	cag	gcc	cat	cag	cct	aat	gtg	tat	gtc	1392	
Ile	Ile	Ser	Lys	Thr	Pro	Gly	Gln	Ala	His	Gln	Pro	Asn	Val	Tyr	Val		
	450					455				460							
ctg	ccg	cca	tcg	cgg	gat	gag	atg	agc	aag	aat	acg	gtc	acc	ctg	acc	1440	
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Met	Ser	Lys	Asn	Thr	Val	Thr	Leu	Thr		
465				470				475				480					
tgt	ctg	gtc	aaa	gac	ttc	ttc	cca	cct	gag	att	gat	gtg	gag	tgg	cag	1488	
Cys	Leu	Val	Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln		
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agc	aat	gga	cag	cag	gag	cct	gag	agc	aag	tac	cgc	atg	acc	ccg	ccc	1536	
Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	Lys	Tyr	Arg	Met	Thr	Pro	Pro		
			500				505					510					
cag	ctg	gat	gaa	gat	ggg	tcc	tac	ttc	cta	tac	agc	aag	ctc	tcc	gtg	1584	
Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val		
	515					520					525						
gac	aag	agc	cgc	tgg	cag	cgg	gga	gac	acc	ttc	ata	tgt	gcg	gtg	atg	1632	
Asp	Lys	Ser	Arg	Trp	Gln	Arg	Gly	Asp	Thr	Phe	Ile	Cys	Ala	Val	Met		
	530				535			540									
cat	gaa	gct	cta	cac	aac	cac	tac	aca	cag	ata	tcc	ctc	tcc	cat	tct	1680	
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Ile	Ser	Leu	Ser	His	Ser		
545				550				555						560			
ccg	ggt	aaa	tga													1692	
Pro	Gly	Lys															

<210> 78  
 <211> 563  
 <212> PRT  
 <213> Canis familiaris

<400> 78  
 Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp  
 1 5 10 15  
 Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
 20 25 30  
 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr

35

40

45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
50 55 60

Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile
65					70					75					80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe  
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser  
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys  
165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys  
180 185 190

Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile
		195					200					205			

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser  
210 215 220

Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro
225					230					235					240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr  
245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln  
260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg  
275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp

290		295		300															
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser				
305					310					315					320				
Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Ala	Lys	Glu	Cys	Glu	Cys	Lys	Cys				
				325					330					335					
Asn	Cys	Asn	Asn	Cys	Pro	Cys	Pro	Gly	Cys	Gly	Leu	Leu	Gly	Gly	Pro				
				340				345					350						
Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Val	Thr	Ala				
		355					360					365							
Arg	Thr	Pro	Thr	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	Glu	Asn				
370						375					380								
Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Ser	Lys	Gln	Val	Gln	Thr				
385					390					395					400				
Ala	Asn	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Ser	Asn	Gly	Thr	Tyr	Arg	Val				
				405					410					415					
Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	Ser	Gly	Lys	Gln				
				420				425					430						
Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	Pro	Ile	Glu	Glu				
		435					440					445							
Ile	Ile	Ser	Lys	Thr	Pro	Gly	Gln	Ala	His	Gln	Pro	Asn	Val	Tyr	Val				
		450				455					460								
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Met	Ser	Lys	Asn	Thr	Val	Thr	Leu	Thr				
465				470						475				480					
Cys	Leu	Val	Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln				
				485					490					495					
Ser	Asn	Gly	Gln	Gln	Glu	Pro	Glu	Ser	Lys	Tyr	Arg	Met	Thr	Pro	Pro				
		500						505					510						
Gln	Leu	Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val				
		515					520					525							
Asp	Lys	Ser	Arg	Trp	Gln	Arg	Gly	Asp	Thr	Phe	Ile	Cys	Ala	Val	Met				
530					535						540								
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Ile	Ser	Leu	Ser	His	Ser				

## Pro Gly Lys

&lt;210&gt; 79

&lt;211&gt; 1692

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 79

tcattttaccc ggagaatggg agagggatat ctgtgtgtag tggttgtgta gagcttcatg 60  
 catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cggagagctt 120  
 gctgtatagg aagtaggacc catcttcate cagctggggc ggggtcatgc ggtacttgct 180  
 ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240  
 tttgaccaga cagggtcaggg tgaccgtatt cttgctcatc tcatcccgcg atggcggcag 300  
 gacatacaca ttaggctgat gggcctgccc tggggctctg gagatgatct cctcaatggg 360  
 ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420  
 gtgcccgaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480  
 ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540  
 gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600  
 gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660  
 tgggcatggg cagttgttac agttacactt gcactcgcat tctttggcca ctggcttgct 720  
 tacttttagtg ttggatccgg tttccttcca gatatcacct ttccagcatt gttcatcact 780  
 ccactcactc cagattccat catctgagca ataaatattc actttacttc ttaccaaaaa 840  
 gcataatttt tggctttcat ttgatgttct tgtgatttgt atctcattct caactgtggg 900  
 agtcacccaa gtagtaccat cctctgtgaa ttcaatttca taaatgaaac atttggctgg 960  
 aatgggtcct ttaggcatgt tccatttcag gttaatttcc tctgaattct tcacagtaag 1020  
 actaaggtag tctggtggca taggtttaac tataatttga agctgaaaaa taaaatagct 1080  
 gggctctgata ggctgggatt ctgatgaccc attaacacag atgtagaaat ctttatagtc 1140  
 tgatgactcc aaatagggaa acctgcatcc catatttttt ccattaacct tgatgtaatc 1200  
 agtacactct gctgaatggg ccaagccctc ataccagtaa aacaactggg aattgggtatc 1260  
 aaaatggaca cccatgccag gtttccaaga gcagactaaa tattgccagt tgtaataatac 1320  
 acagtccata tcttgaattt tagtttcccc atttccttgt ggtgatgtcc aataagtagt 1380  
 ttctgccccat gaacttctaa cttctgatcc atttgtgcat tgtgctggca gaagtgtgtt 1440  
 tatctttgct tcaatacctt tgtaagatc aaaccctct ttgtaatgta gattcttggg 1500  
 aatgatggtc ttccagtttt cactatcaat gtttcgggat tttaattcat attctattgt 1560  
 gcattcctta aaattatccg gaaataatgg aggttgccat tgcaaagaga gataacctaa 1620  
 atatccaggg tccactatct caaaatcctg aggaggatta acttttatct cagcatttga 1680  
 aagcatagac at 1692

&lt;210&gt; 80

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

<220>

<221> CDS

<222> (1)..(1683)

<400> 80

atg tct atg ctt tca aat gct gag ata aaa gtt aat cct cct cag gat	48
Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp	
1 5 10 15	
ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg	96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
20 25 30	
caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile	
50 55 60	
acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att	240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile	
65 70 75 80	
gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca	288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser	
85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	

175

atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc 1104  
Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro



	355						360						365						
gag	atc	acc	tgt	gtg	gtg	tta	gat	ctg	ggc	cgt	gag	gac	cct	gag	gtg	1152			
Glu	Ile	Thr	Cys	Val	Val	Leu	Asp	Leu	Gly	Arg	Glu	Asp	Pro	Glu	Val				
370						375						380							
cag	atc	agc	tgg	ttc	gtg	gat	ggg	aag	gag	gtg	cac	aca	gcc	aag	acg	1200			
Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Glu	Val	His	Thr	Ala	Lys	Thr				
385						390						395			400				
cag	cct	cgt	gag	cag	cag	ttc	aac	agc	acc	tac	cgt	gtg	gtc	agc	gtc	1248			
Gln	Pro	Arg	Glu	Gln	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val				
			405						410						415				
ctc	ccc	att	gag	cac	cag	gac	tgg	ctc	acc	gga	aag	gag	ttc	aag	tgc	1296			
Leu	Pro	Ile	Glu	His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Glu	Phe	Lys	Cys				
			420						425						430				
aga	gtc	aac	cac	ata	ggc	ctc	ccg	tcc	ccc	atc	gag	agg	act	atc	tcc	1344			
Arg	Val	Asn	His	Ile	Gly	Leu	Pro	Ser	Pro	Ile	Glu	Arg	Thr	Ile	Ser				
435						440						445							
aaa	gcc	aga	ggg	caa	gcc	cat	cag	ccc	agt	gtg	tat	gtc	ctg	cca	cca	1392			
Lys	Ala	Arg	Gly	Gln	Ala	His	Gln	Pro	Ser	Val	Tyr	Val	Leu	Pro	Pro				
450						455						460							
tcc	cca	aag	gag	ttg	tca	tcc	agt	gac	acg	gtc	acc	ctg	acc	tgc	ctg	1440			
Ser	Pro	Lys	Glu	Leu	Ser	Ser	Ser	Asp	Thr	Val	Thr	Leu	Thr	Cys	Leu				
465						470						475			480				
atc	aaa	gac	ttc	ttc	cca	cct	gag	att	gat	gtg	gag	tgg	cag	agc	aat	1488			
Ile	Lys	Asp	Phe	Phe	Pro	Pro	Glu	Ile	Asp	Val	Glu	Trp	Gln	Ser	Asn				
			485						490						495				
gga	cag	ccg	gag	ccc	gag	agc	aag	tac	cac	acg	act	gcg	ccc	cag	ctg	1536			
Gly	Gln	Pro	Glu	Pro	Glu	Ser	Lys	Tyr	His	Thr	Thr	Ala	Pro	Gln	Leu				
			500						505						510				
gac	gag	gac	ggg	tcc	tac	ttc	ctg	tac	agc	aag	ctc	tct	gtg	gac	aag	1584			
Asp	Glu	Asp	Gly	Ser	Tyr	Phe	Leu	Tyr	Ser	Lys	Leu	Ser	Val	Asp	Lys				
515						520						525							
agc	cgc	tgg	cag	cag	gga	gac	acc	ttc	aca	tgt	gcg	gtg	atg	cat	gaa	1632			
Ser	Arg	Trp	Gln	Gln	Gly	Asp	Thr	Phe	Thr	Cys	Ala	Val	Met	His	Glu				
530						535						540							
gct	cta	cag	aac	cac	tac	aca	gat	cta	tcc	ctc	tcc	cat	tct	ccg	ggg	1680			
Ala	Leu	Gln	Asn	His	Tyr	Thr	Asp	Leu	Ser	Leu	Ser	His	Ser	Pro	Gly				

545

550

555

560

aaa tga

1686

Lys

&lt;210&gt; 81

&lt;211&gt; 561

&lt;212&gt; PRT

&lt;213&gt; Canis familiaris

&lt;400&gt; 81

Met Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn Pro Pro Gln Asp  
 1 5 10 15

Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp  
 20 25 30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr  
 35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile  
 50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile  
 65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser  
 85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln  
 100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn  
 115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe  
 130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser  
 145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys  
 165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys  
 180 185 190

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Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro  
 450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu  
 465 470 475 480

Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn  
 485 490 495

Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu  
 500 505 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys  
 515 520 525

Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu  
 530 535 540

Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly  
 545 550 555 560

Lys

<210> 82  
 <211> 1686  
 <212> DNA  
 <213> Canis familiaris

<400> 82  
 tcattttaccc ggagaatggg agaggggatag atctgtgtag tggttctgta gagcttcatg 60  
 catcaccgca catgtgaagg tgtctccctg ctgccagcgg ctcttggtcca cagagagctt 120  
 gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180  
 ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcagggtg ggaagaagtc 240  
 tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatgggtgg 300  
 caggacatac aactgggct gatgggcttg cctctggct ttggagatag tcctctcgat 360  
 gggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc 420  
 ctggtgctca atggggagga cgctgaccac acggtaggtg ctggtgaact gctgctcacg 480  
 aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540  
 agggctcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600  
 gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660  
 gactgggcat ggggatatac acttgacagg ggactctttg ggactgggt tgtctacttt 720  
 agtgttggat ccggtttcct tccagatatc acctttccag cattgttcat cactccactc 780  
 actccagatt ccatcatctg agcaataaat attcacttta cttcttacca aaaagcataa 840  
 tttttggctt tcatttgatg ttcttgatg ttgtatctca ttctcaactg tggtagtcac 900  
 ccaagtagta ccatcctctg tgaattcaat ttcataaatg aaacatttgg ctggaatggg 960

tccttttaggc atgttccatt tcagggttaat ttctcttgaa ttcttcacag taagactaag 1020  
 gtagtctggg ggcataagggt taactatatatt ttgaagctga aaaataaaat agctgggtct 1080  
 gataggctgg gattctgatg acccattaac acagatgtag aaatctttat agtctgatga 1140  
 ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200  
 ctctgctgaa tgggtccaagc cctcatacca gtaaaacaac tggtaattgg tatcaaaatg 1260  
 gacacccatg ccagggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320  
 catatcttga attttagttt cccgatttcc ttgtggtgat gtccaataag tagtttctgc 1380  
 ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440  
 tgcttcaata cctttgttaa gatcaaacc atctttgtaa tgtagattct tggtaatgat 1500  
 ggtcttccag ttttcaactat caatgtttcg gtattttaat tcatattcta ttgtgcattc 1560  
 cttaaaatta tccggaaata atggagggtt ccattgcaaa gagagataac ctaaatatcc 1620  
 aggggtccact atctcaaaat cctgaggagg attaactttt atctcagcat ttgaaagcat 1680  
 agacat 1686

<210> 83

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<223> At locations 9, 18, 21 and 27, n = unknown

<400> 83

athtggacnt ggaayccncc ngarggngc 29

<210> 84

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<223> At locations 6, 9, 21 and 33, n = unknown

<400> 84

atyttncng crttrtctyt naccatdaty tgnac 35

<210> 85

<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<223> At locations 12, 18 and 21, n = unknown

<400> 85  
garathaarg tnaayccncc ncargaytty garat

35

<210> 86  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<223> At locations 12, 22 and 31, n = unknown

<400> 86  
tayaargayg gnttctgayy tnaayaargg nathga

36

<210> 87  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<220>  
<223> At locations 7, 16, 25 and 40, n = unknown

<400> 87  
ccaytcnswc cadatncert crtngcrca rtadatrttn acytt

45

<210> 88

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<220>

<223> At locations 9 and 12, n = unknown

<400> 88

gertgrtcna rncctcrta cca

23

<210> 89

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 89

agcggatccc tctatgcttt caaatgctga gataaaagtt aatcctcctc agg

53

<210> 90

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 90

tggacatcac cacaaggaaa tcggg

25

<210> 91

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 91  
gcacatatgt ctatgctttc aaatgctgaa taaaagttaa tcctcctcag g 51

<210> 92  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 92  
aaaggatccg gtttccttcc agatatcatt tccage 36

<210> 93  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 93  
ccgggatcca acactaaagt agacaagcgt g 31

<210> 94  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 94  
gcgctcgagt catttaccg gagaatggga ggg 33

<210> 95  
<211> 1525  
<212> DNA



<213> Canis familiaris

<400> 95

gaattcggca cgaggggagag gaggagggaa agatagaaag agagagagaa agattgcttg 60  
ctaccctga acagtacac ctctcaagac agtgctttgc tcttcacgta taaggaagga 120  
aaacagtaga gattcaattt agtgtctaag gtggaaagga ggacaaagag gtcttgtgat 180  
aactgcctgt gataatacat ttcttgagaa accatattat tgagtagagc tttcagcaca 240  
ctaaatcctg gagaaatggc ttttgtgcat atcagatgct tgtgtttcat tcttctttgt 300  
acaataactg gctattcttt ggagataaaa gttaatcctc ctcaggattt tgaaatattg 360  
gatectggat tacttggtta tctctatttg caatggaaac ctctgtggt tatagaaaaa 420  
tttaagggct gtacactaga atatgagtta aaataccgaa atgttgatag cgacagctgg 480  
aagactataa ttactaggaa tctaatttac aaggatgggt ttgatcttaa taaaggcatt 540  
gaaggaaaga tacgtacgca tttgtcagag cattgtacaa atggatcaga agtacaaagt 600  
ccatggatag aagcttctta tgggatatca gatgaaggaa gtttggaac taaaattcag 660  
gacatgaagt gtatatatta taactggcag tatttggctt gctcttgga acctggcaag 720  
acagtatatt ctgataccaa ctataccatg ttttctggt atgagggctt ggatcatgcc 780  
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gaattccttc atattagtgt ggagaattcc attgatatta gaatgaaatg gagcacacct 1020  
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tgtgcttatg aagataccct ctgttaaacc accaatttct tgacatagag ccagccagca 1440  
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<210> 96

<211> 1369

<212> DNA

<213> Canis familiaris

<400> 96

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gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac ttcattctca 180  
gacaccgaga taaaagttaa cctcctcag gattttgaga tagtggatcc cggatactta 240  
ggttatctct atttgcaatg gcaaccccca ctgtctctgg atcattttta ggaatgcaca 300  
gtggaatatg aactaaaata ccgaaacatt ggtagtgaag catggaagac catcattact 360  
aagaatctac attacaaaga tgggtttgat cttaacaagg gcattgaagc gaagatacac 420  
acgcttttac catggcaatg cacaatgga tcagaagttc aaagttcctg ggcagaaact 480  
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tattacaatt ggcaatattt actctgttct tggaaacctg gcataggtgt acttcttgat 600  
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agagacatgg tattgactca acagtttcca gtcattggcca aatgttcaat atgagtctca 1320  
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<210> 97

<211> 1525

<212> DNA

<213> Canis familiaris

<400> 97

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aacagagggg atcttcataa gcacacactt ctttggttcag atccacatgg aggctcaatg 180  
tgggttcagg ttcttccttc tccacaataa ggcaaagaag taacaaaagg aatataaaga 240  
aaagacaaac tggactatg aaaataatct ttgagtctgg ccctgtgtaa ctttcccaac 300  
attcctcttc actccattcg ctccaaattc catcatctgc acaatatata ttgaccttac 360  
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ttttgtctgt ggcagactcc caggaaatat cgtcttctcg gatcacaatt tcataagtgt 480  
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acactaaatt gaatctctac tgttttcctt ccttatacgt gaagagcaaa gcaactgtctt 1440  
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<210> 98  
 <211> 1369  
 <212> DNA  
 <213> Canis familiaris

<400> 98  
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 gtcttcatgt atcacagaaa aattctggaa tcatttttgg gtaggtgttt ggcttacgca 180  
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 aagccatttc tccgagattt aaaaccttga tattgcctct ctccccgccg acaggcacac 1320  
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<210> 99  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 99  
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27

<210> 100  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 100

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27

<210> 101

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 101

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21

<210> 102

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 102

cgggctggct ccctcgggag g

21

<210> 103

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 103

catggtcccc ggcgttcttc c

21

<210> 104

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 104

ggtgagaata ccgacccac g

21

109